

71264

LB

STIC-Biotech/ChemLib

From: Davis, Minh-Tam  
Sent: Thursday, July 18, 2002 9:53 AM  
To: STIC-Biotech/ChemLib  
Subject: Search request for 09/840746

Please search in commercial database and in issued patent files:

1) SEQ ID NOs: 1 and 2

Thank you.

MINH TAM DAVIS

ART UNIT 1642, ROOM 8A01, MB 8E12

305-2008

priority date  
4/01

Point of Contact  
P. Sheppard  
Telephone number: (703) 308-4499

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: 7/26/02  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:

NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
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WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 25, 2002, 19:34:16 ; Search time 12075.4 Seconds  
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Title: US-09-840-746-2

Perfect score: 6952  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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33: em\_hgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5098.4	73.3	6407	6	AR065869	AR065869 Sequence
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5	1438.8	20.7	1462	9	BC004539	BC004539 Homo sapi
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13	263.4	3.8	34308	9	AF389852	AF389852 Homo sapi
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ALIGNMENTS

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DEFINITION Homo sapiens mRNA for KIAA1237 protein, partial cds.  
ACCESSION AB033063  
VERSION AB033063.1 GI:6330761  
KEYWORDS  
SOURCE Homo sapiens brain cDNA to mRNA, clone\_id:pb1uescriptII SK plus  
clone:fh09696.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE  
1 (sites) Nagase,T., Ishikawa,K., Kikuno,R., Hirotsawa,M., Nomura,N. and  
Ohara,O.  
TITLE Prediction of the coding sequences of unidentified human genes. XV.  
The complete sequences of 100 new cDNA clones from brain which code  
for large proteins in vitro  
JOURNAL DNA Res. 6 (5), 337-345 (1999)  
MEDLINE 2 (bases 1 to 5142)  
REFERENCE Ohara,O., Nagase,T. and Kikuno,R.  
AUTHORS Direct Submission  
TITLE

Submitted (04-Oct-1999) Osamu Ohara, Kazusa DNA Research Institute,  
Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba  
292-0812, Japan (E-mail:cdna@kazusa.or.jp)  
URL: http://www.kazusa.or.jp/huge/, Tel: +81-438-52-3913,  
Fax: +81-438-52-3914)

FEATURES

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	Query Match	Length DB	ID	Description
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	6	470.4	6.8	584	4	US-09-328-111-83
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39	44.8	0.6	9636	1	US-08-954-441-1	Sequence 1, Appl1
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41	44.2	0.6	5163	3	US-08-928-361B-4	Sequence 1, Appl1
42	44.2	0.6	5318	3	US-08-700-651-2	Sequence 2, Appl1
43	44.2	0.6	5318	3	US-08-928-361B-3	Sequence 3, Appl1
44	43.6	0.6	43795	3	US-08-742-185-101	Sequence 101, App

#### ALIGNMENTS

RESULT 1  
US-08-616-844-7  
Sequence 7, Application US/08616844  
Patent No. 5849578  
GENERAL INFORMATION:  
APPLICANT: FALB, DEAN A.  
TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/616,844  
FILING DATE: 15-MAR-1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/599,654  
FILING DATE: 09-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,573  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CORUZZI, LAURA A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-053  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6407 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: unknown  
MOLECULE TYPE: cDNA  
US-08-616-844-7









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Dh	5646	ATPACTTTTKTTTCTCACCCAGTCACTTGTACTCTTCTATATAGGSTATGTGCACACCTCC	5705
	4740	agaaacgttgattatacttccagctcagctgtgtggaagacccaagacttcgggttgtgcagg	4799
Dh	5706	AGAAAACGTGGTATACTKCCACTGATGTTGGGAGAACCTGAACACTTCCGGTGTGCGAGG	5765
Oy	4800	aacttgaaggttaccttctgggaaggaagttccacatcatctattatatactcctgttga	4859
Dh	5766	AACTAGAGGTTTACTTGTGGGAAGAACTTCCACTCATCTTATTTATATACCGTATAG	5825
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RESULT 2  
 US-08-599-654-7  
 Sequence 7, Application US/08599654  
 Patent No. 5882925  
 GENERAL INFORMATION:  
 APPLICANT: FALB, DEAN A  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
 TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
 NUMBER OF SEQUENCES: 54  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PENNIE & EDMONDS  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10036-2711  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/599,654  
 FILING DATE: 09-FEB-1996  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/485,573  
 FILING DATE: 07-JUN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/386,844  
 FILING DATE: 10-FEB-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: CORUZZI, LAURA A  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 7853-041  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-8864  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID: NO. 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6407 base-pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: unknown  
 MOLECULE TYPE: CDNA

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 25, 2002, 19:34:16 ; Search time 12075.4 Seconds

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_htg: \*  
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7: gb\_ph: \*  
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30: em\_htg\_hum: \*  
31: em\_htg\_inv: \*  
32: em\_htg\_other: \*  
33: em\_htgo\_inv: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	3500.6	50.4	110000	2	AC092983_0	AC092983 Homo sapi
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16	126.4	1.8	128	6	AR148306	AR148306 Sequence
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18	102.6	1.5	2008	9	AB062989	AB062989 Macaca fa
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## ALIGNMENTS

RESULT 1  
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LOCUS AB033063  
DEFINITION Homo sapiens mRNA for KIAA1237 protein, partial cds.  
ACCESSION AB033063  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE  
AUTHORS Nagase,T., Ishikawa,K., Kikuno,R., Hirosewa,M., Nomura,N. and Ohara,O.  
TITLE Prediction of the coding sequences of unidentified human genes. XV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro  
JOURNAL DNA Res. 6 (5), 337-345 (1999)  
MEDLINE 20039619  
REFERENCE 2 (bases 1 to 5142)  
AUTHORS Ohara,O., Nagase,T. and Kikuno,R.  
TITLE Direct Submission

**JOURNAL**  
**FEATURES**  
**SOURCE**

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/protein_id="P12345" protein
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/db_xref="GI:6330762"
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CNLVRTEFVTEFKLKRTFLNTTV

KRKSP ECDKDT SICTDL DGVA

GLGG LNCGNFIQULI V VIATAC  
PYAFY PKNPRSQEWGBEATFME

1317 C 1348 C

tv	100.0%	pred	score	15.38
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derivative  $U$ ; Mismat

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TTTCTGTCTCACAAACCTT

qqqaaactcctatgaattcat

[illegible][illegible]

ATAGTAGTCAAAAC TGCAGAC

cagaatcaagtcaccaagcc

CAGAATCAAAGTCACCAAGCC

caactctccttqcctccat

CADACCTTCCTCCTCCCTA

11111111111111111111

**APPENDIX C**

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TACCTACAGACTACCTC

al 20

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Oy 4353 tctatcaccaatgttgaagccagagcagctgtgagccctgagcgtgagtgtgtag 4472  
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Db 3721 AAAAGGAAACTGTTTATCAGTGAAGGTAACTAAATTTCAAAAGTGTGCTTTT 3780



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 25, 2002, 20:03:31 ; Search time 192.67 Seconds

(without alignments)  
8863.051 Million cell updates/sec

Title: US-09-840-746-2

Perfect score: 6952

Sequence: 1 gtcgatgaagaatgcgcgtacgtgggaagctataggatg 6952

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, NA.\*

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3: /cgn2\_6/ptodata/2/lna/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/2/lna/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/2/lna/PCRTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/2/lna/Backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5098.4	73.3	6407	2	US-08-616-844-7
2	5098.4	73.3	6407	2	US-08-599-654-7
3	5098.4	73.3	6407	3	US-08-944-868A-7
4	5098.4	73.3	6407	3	US-08-944-823A-7
5	5098.4	73.3	6407	3	US-08-944-496-7
6	470.4	6.8	584	4	US-09-328-111-83
7	126.4	1.8	128	2	US-08-480-994-7
8	126.4	1.8	128	2	US-08-485-573-7
9	126.4	1.8	128	3	US-08-925-743-7
10	126.4	1.8	128	3	US-08-925-767-7
11	89.8	1.3	7218	1	US-08-232-463-14
12	56.2	0.8	3489	2	US-08-728-323A-1
13	56.2	0.8	32207	2	US-08-770-379-20
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18	48.8	0.7	289	4	US-09-007-005-17
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20	48.8	0.7	696	4	US-09-461-697-193
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22	48.8	0.7	717	4	US-09-461-697-189
23	48.8	0.7	774	4	US-09-461-697-187
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29	48.2	0.7	3211	4	US-09-357-014-8	Sequence 8, Appl 1
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35	46.6	0.7	1052	2	US-08-466-717-1	Sequence 1, Appl 1
36	46.6	0.7	1052	2	US-08-466-743-1	Sequence 1, Appl 1
37	46.6	0.7	1052	5	PCT-US95-12414-1	Sequence 11, Appl 1
38	46.6	0.7	18596	4	US-09-318-448-11	Sequence 1, Appl 1
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42	44.2	0.6	5163	3	US-08-928-361B-4	Sequence 2, Appl 1
43	44.2	0.6	5318	3	US-08-700-651-2	Sequence 3, Appl 1
44	44.2	0.6	5318	3	US-08-928-361B-3	Sequence 101, App
45	43.6	0.6	43795	3	US-08-742-185-101	

#### ALIGNMENTS

RESULT 1  
US-08-616-844-7  
Sequence 7, Application US/08616844  
Patent No. 5849578

GENERAL INFORMATION:  
APPLICANT: FALB, DEAN A.  
TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESS: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/616,844  
FILING DATE: 15-MAR-1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/599,654  
FILING DATE: 09-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,573  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CORRUZZI, LAURA A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-053  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6407 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA  
US-08-616-844-7



Query Match 73.38; Score 5098.4; DB 2; Length 6407;  
 Best Local Similarity 94.38; Pred. No. 0;  
 Matches 5412; Conservative 21; Mismatches 8; Indels 301; Gaps 2;

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 DB 786 GGCCTTGAGCCCGCTCTTCTTCTCTGATGGAGATGGAGACTTACACAGGCTTCTAG 845  
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 DB 966 TGGCTCCAGAGCTCTCTCAGTCACTCAACAAAGAACATGATGTTGCTACCTGCTTAC 1025  
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 DB 1806 GGCCATGCCCAAGAAAGAGAGGCTCTCTGCACTTAAACGTACGAGACAGACTGGG 1865  
 QY 941 ----- 1092ggtgattagctacg 959  
 DB 1866 CCTGTCTACGCTACTGCGCCCTCAGTGCACATCGGAGTGGGTAGGTAGCTACGG 1925  
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 QY 1020 cctgtcatctacttccacaagagagagcggttactgttcatctaaagataaagttc 1079  
 DB 1986 CCTGTCACTACTTTCACCAAGAGAACGGCGTTACTGTCTCAATTAAGATTAACAGTT 2045  
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 DB 2286 TAGTGAATCCT 2345  
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Db	3846	GTGCAAGCGGAAGACTCCCGAATGTGAAAGACACCCTCATCTGCACCTGCAGCG	390
OY	2940	CGTTCGCCGTGTCCAGTTCGAAGTCGGATCTCTTCAGTTCGAAGAATGACCACTCTG	299
Db	3906	CGTTCGCCGTGTCCAGTTCGAAGTCGGATCTCTTCAGTTCGAAGAATGACCACTCTG	366
OY	3000	CCGAGCATGTGAAGAATGATATAGCTTGAAGAAATGAACCTGCATGATGCTCCATTTGG	402
Db	3966	CCGAGCATGTGAAGATGATATAGCTTGAAGAAATGAACCTGCATGATGCTCCATTTGG	402
OY	3060	CCCTTGTGTCTCAACTGTGAAACCCCTATCACCTTATCATCTGTGTGATCCGACGCCG	408
Db	4026	CCCTTGTGTCTCAACTGTGAAACCCCTATCACCTTATCATCTGTGTGATCCGACGCCG	408
OY	3120	GGGAGGTGGGCTCCTGCTCATCTCAGGATGCACTGATTTGACCTGTTGCACAAAAAA	414
Db	4086	GGGAGGTGGGCTCCTGCTCATCTCAGGATGCACTGATTTGACCTGTTGCAAAAAAA	414
OY	3180	TAAATAATGACATTAAGCAAACTCATCTTCAAAAGTGGAGATTCCAAATGCCCCATATGC	420
Db	4146	TAAATAATGACATTAAGCAAACTCATCTTCAAAAGTGGAGATTCCAAATGCCCCATATGC	420
OY	3240	TGAATATCCCAAAAAATCTCCCTCACAAGATGGGCGGAGAGCTATTGAAATGTCATGA	426
Db	4206	TGAATATCCCAAAAAATCTCCCTCACAAGATGGGCGGAGAGCTATTGAAATGTCATGA	426
OY	3300	GAATGAGATCAACAAAACCTCCTCCAGATGACGATGTGACTACTGCTTCAAAAGTGT	432
Db	4266	GAATGAGATCAACAAAACCTCCTCCAGATGACGATGTGACTACTGCTTCAAAAGTGT	432
OY	3360	AAGGAATCCAGAACTTGAACGAACAGGACTACCCGCTACACTGACATGTCAGAGATC	438
Db	4326	AAGGAATCCAGAACTTGAACGAACAGGACTACCCGCTACACTGACATGTCAGAGATC	438
OY	3420	ACGGATCTCTGCATTTCCCGGACAGTAAACCCCTTTTCATCATGATGATGAAAGCAG	444
Db	4386	ACGGATCTCTGCATTTCCCGGACAGTAAACCCCTTTTCATCATGATGATGAAAGCAG	444
OY	3480	AAGAAGAGACTACTTTAAAGTCCGAGGAGAGAGGAGGACTATGCTCTGAGCCAGTACAC	353
Db	4446	AAGAAGAGACTACTTTAAAGTCCGAGGAGAGAGGAGGACTATGCTCTGAGCCAGTACAC	353
OY	3540	TGGGACCTCTGCTCAGAGAACCGGACAGGAGGCTGCGCCAGGATTTGTCCGGAGCCAC	456
Db	4506	TGGGACCTCTGCTCAGAGAACCGGACAGGAGGCTGCGCCAGGATTTGTCCGGAGCCAC	456
OY	3600	GCTGATGTGGCAACGACGAGAAAGGAGACAGCATCCGGGCTGTACACAGTGGAGGAGACA	462
Db	4566	GCTGATGTGGCAACGACGAGAAAGGAGACAGCATCCGGGCTGTACACAGTGGAGGAGACA	462
OY	3660	GTGTGATGTGGCAACGACGCTGCTCATTTAGACACTTGTGTTACTGTGAACGTGAAT	468
Db	4626	GTGTGATGTGGCAACGACGCTGCTCATTTAGACACTTGTGTTACTGTGAACGTGAAT	468
OY	3720	GTGGGCAAGATCAAGAGATCTCTCTGATGACTCCACATGAGCACTGTGGCAACGAGCG	474
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OY	3780	ACTATATGACGAGGACAGACCACTAAGACTTCAAGGACGAGGACCTGCTTCTGCTTGG	480
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OY	3840	CACCTTATGATTAATGGGTGTGGAGTTTCCCTTGTGGATCTGTTTGAAGTGTTCAGAAA	486
Db	4806	CACCTTATGATTAATGGGTGTGGAGTTTCCCTTGTGGATCTGTTTGAAGTGTTCAGAAA	486
OY	3900	GAAGGCTCTCTTCCGAGACACTTCCATTAAGGACGAGCAATTTGGTATTCAATTCASCAA	492
Db	4866	GAAGGCTCTCTTCCGAGACACTTCCATTAAGGACGAGCAATTTGGTATTCAATTCASCAA	492
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 Db 4986 TGASGCTACCACTGAAAGTCTGAAGATGCTGCCATGAAAGGACATGTTTTCATATGTTT 5045  
 QY 4080 ctgaagttcttaagctcagttccaaagccagcccccacagtgaggaatggttgaagc 4139  
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 Db 5286 TCAATCATGAGGGCCAGCTTGGGCTGGGACTGATCAGATTCATGAGGAGGCGAGAGG 5345  
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 Db 5346 CAMCTGCGATGAGGAGGAATGTCAAACTGAACGAGTTTACACACTCTAGGAAAGA 5405  
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 Db 5586 CATGTCCAAACCCCAATGAACTTTCAACACACACACACACACACACACACACACACAC 5645  
 QY 4680 ataacttttttccac 4739  
 Db 5646 AATACTTTTCTTCTACCCAGTCTATTGTACTTCTCATATGATGATGATGATGATGATG 5705  
 QY 4740 agaacgtggtataactcagtcagtgtagtggaagacacacacacacacacacacacac 4799  
 Db 5706 AGAAGCTGTTTACTACACAGTCTGAGTGGGAGAACAGAGACTTCCGTTGGTGGAGG 5765  
 QY 4800 aacgaggtgagctcaggaagaagacacacacacacacacacacacacacacacacacac 4859  
 Db 5766 AACGAGGCTTGAACCTTGGGAGGAAGTTCCACTCATCTTATTTATATATATATATATAT 5825  
 QY 4860 tgggtctgacaggaagac 4919  
 Db 5826 TGGGTCTGACAGGAGACATCCAGTCTGCTCTCTATTTGCTCACTGAGGAGACTGT 5885  
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 Db 5886 GTTATTGAGCTTCTTGGGAGCATCTGCTGATGAGTGAAGTGAAGGAGGAGTACAGAGTA 5945  
 QY 4980 aagaattgctccac 5039  
 Db 5946 AAGGAATGCTCTACACCTGAAAGCGGAGATCCCGCTTCAATTTTGAAGATGCTGACAG 6005  
 QY 5040 caactggagacagttctgcccggagagtggtttcttaaggtctcctaataatc 5099  
 Db 6006 CCACTGGGAGCATCTGCCCCGGGAGATGTTTCTTCAAGTCTCTCAATATATATATATAT 6065

QY 5100 cctattctacataatccttgccctgagtggtttaagcaagaacacacacacacacacacac 5159  
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RESULT  
 2  
 US-08-599-654-7  
 ; Sequence 7, Application US/08599654  
 ; Patent No. 5882925  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FALB, DEAN A  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
 ; TITRATION OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
 ; NUMBER OF SEQUENCES: 34  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: PENNIE & EDMONDS  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/599,654  
 ; FILING DATE: 09-FEB-1996  
 ; CLASSIFICATION: 800  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/485,573  
 ; FILING DATE: 07-JUN-1995  
 ; PRIOR APPLICATION DATA:  
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 ; ATTORNEY/AGENT INFORMATION:  
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 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 6407 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: both  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: cDNA  
 ; US-08-599-654-7

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